

WHAT IS CLAIMED IS:

1                   1.     A method of detecting cancer in a patient, the method comprising:  
2                   determining the level of a transcript encoding SEQ ID NO:2 in a biological  
3 sample from the patient; and  
4                   detecting a decrease in the level of the transcript relative to normal, thereby  
5 detecting the presence of cancer in the patient.

1                   2.     The method of claim 1, wherein the cancer is selected from a group  
2 consisting of lung cancer, breast cancer, mesothelioma, colon cancer, and sarcoma.

1                   3.     The method of claim 1, wherein the step of determining the level of the  
2 transcript comprises an amplification reaction.

1                   4.     A method of detecting cancer in a patient, the method comprising:  
2                   determining the level of a polypeptide having the sequence set forth in SEQ  
3 ID NO:2 in a biological sample from the patient; and  
4                   detecting an increase in the level of the polypeptide relative to normal, thereby  
5 detecting the presence of cancer in the patient.

1                   5.     The method of claim 4, wherein the cancer is selected from the group  
2 consisting of lung cancer, breast cancer, mesothelioma, colon cancer, and sarcoma.

1                   6.     The method of claim 4, wherein the step of determining the level of the  
2 polypeptide comprises performing an immunoassay.

1                   7.     A method of detecting cancer in a patient, the method comprising:  
2                   determining the amount of methylation of a SOCS-3 promoter in a biological  
3 sample from the patient; and  
4                   detecting an increase in the amount of methylation of the sample relative to  
5 normal, thereby detecting the presence of cancer in the patient.

1                   8.     The method of claim 7, wherein the amount of methylation of the CpG  
2 residues that occur within the region from -1005 to -983 or from -754 to -737 of SEQ ID  
3 NO:3 is determined.

1                   9.     The method of claim 7, wherein the amount of methylation of the  
2 SOCS-3 promoter is determined using bisulfite sequencing.

1                   10.    The method of claim 7, wherein the amount of methylation of the  
2 SOCS-3 promoter is determined using methylation-specific PCR.

1                   11.    The method of claim 7, wherein the amount of methylation is detected  
2 using a methylation-sensitive restriction enzyme.

1                   12.    A method of monitoring the efficacy of a therapeutic treatment of  
2 cancer, the method comprising the steps of:

3                   (i) providing a biological sample from a patient undergoing the therapeutic  
4 treatment; and

5                   (ii) detecting the level of: a polypeptide having an amino acid sequence of  
6 SEQ ID NO:2, or of a nucleic acid that encodes the polypeptide, in the biological sample  
7 compared to a level in a biological sample from the patient prior to, or earlier in, the  
8 therapeutic treatment, thereby monitoring the efficacy of the therapy.

1                   13.    A method of monitoring the efficacy of a therapeutic treatment of  
2 cancer, the method comprising the steps of:

3                   (i) providing a biological sample from a patient undergoing the therapeutic  
4 treatment; and

5                   (ii) detecting the level of methylation of the SOCS-3 promoter in the  
6 biological sample compared to a level in a biological sample from the patient prior to, or  
7 earlier in, the therapeutic treatment, thereby monitoring the efficacy of the therapy.

1                   14.    A method of screening for an agent that increases SOCS-3 activity, the  
2 method comprising

3                   incubating a test compound with a cell comprising a SOCS-3 nucleic acid  
4 having at least 80% identity to SEQ ID NO:1;

5                   selecting a compound that increases SOCS-3 activity, thereby identifying an  
6 agent that increases SOCS-3 activity.

1                   15.    The method of claim 14, wherein the SOCS-3 nucleic acid sequence  
2 further comprises a hypermethylated promoter.

1                   16.     The method of claim 15, further comprising a step of determining the  
2 amount of methylation of the SOCS-3 promoter following incubation with the test  
3 compound.

1                   17.     The method of claim 14, wherein the increase in SOCS-3 activity is  
2 determined by measuring the level of SOCS-3 mRNA transcript.

1                   18.     The method of claim 14, wherein the increase in SOCS-3 activity is  
2 determined by measuring the level of SOCS-3 polypeptide.

1                   19.     A method of inhibiting proliferation of a cancer cell, the method  
2 comprising administering an agent that increases SOCS-3 activity to the cancer cell.

1                   20.     The method of claim 19, wherein the cancer cell has a hypermethylated  
2 SOCS-3 promoter.

1                   21.     The method of claim 20, wherein the cancer cell is selected from the  
2 group consisting of a lung cancer cell, a breast cancer cell, a mesothelioma cell, a colon  
3 cancer cell, and a sarcoma cell.

1                   22.     The method of claim 19, wherein the agent is an expression vector  
2 encoding SOCS-3.

1                   23.     The method of claim 19, wherein the agent is recombinant SOCS-3.

1                   24.     The method of claim 19, wherein the agent is a demethylating agent.

1                   25.     A kit comprising methylation-specific primers that are selective for  
2 methylated residues present within the region from -1005 to -983 or from -754 to -737 of  
3 SEQ ID NO:3.

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